

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2002, 12:23:18 : Search time 39.0266 Seconds
(without alignments)
3273.388 Million cell updates/sec

Title: US-10-054-680-4

Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGVLTVL.....ADYGRGGGDRSDRGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3093	95.8	924	4	Q96G01
2	3093	95.8	924	4	Q96G02
3	3012	93.3	595	11	Q9EP08
4	3012	93.3	928	11	Q9VH08
5	2157	66.8	934	6	Q97801
6	2156.5	66.8	941	6	Q28662
7	2154.5	66.7	602	6	Q9TV05
8	2136.5	66.2	941	6	Q9TS14
9	2133	66.1	934	11	Q9R238
10	2131	66.0	934	11	Q9WU30
11	2129	65.9	957	11	Q9R239
12	2128.5	65.9	600	11	Q912J7
13	2126.5	65.8	600	11	Q9ET74
14	2124	65.8	962	11	Q924Y2
15	2124	65.8	969	11	Q9WU29
16	2102	65.1	583	13	Q91850

17	2099.5	65.0	940	11	Q35157	035157 mus musculu
18	2030	62.9	968	13	Q9PT19	09PT19 oncorhynch
19	1501	46.5	892	5	Q02196	002196 loligo opal
20	1339.5	41.5	950	5	Q24413	024413 drosophila
21	1339.5	41.5	950	5	Q9VDS5	09VDS5 drosophila
22	1328	41.1	950	5	Q18367	018367 drosophila
23	1288	39.9	925	5	Q45630	045630 caenorhabd
24	1285.5	39.8	925	5	Q94161	094161 caenorhabd
25	1278	39.6	254	13	Q9VH83	09VH83 gallus gall
26	1278	39.6	793	4	Q9H021	09H021 homo sapien
27	1160	35.9	880	5	Q21609	021609 caenorhabd
28	1105.5	34.2	263	13	Q9YGE0	09YGE0 oncorhynch
29	1046.5	32.4	263	13	Q9YH84	09YH84 gallus gall
30	1038	32.2	264	13	Q9YGE1	09YGE1 oncorhynch
31	970.5	30.1	267	13	Q9YGE2	09YGE2 oncorhynch
32	660	20.4	199	11	Q8R505	08R505 mus musculu
33	655	20.3	560	13	Q91849	091849 xenopus lae
34	633.5	19.6	807	5	Q21895	021895 caenorhabd
35	523.5	16.2	171	11	Q8R504	08R504 mus musculu
36	519	16.1	215	11	Q9Z0T8	09Z0T8 ratus norv
37	487	15.1	158	6	Q9MY54	09MY54 oryctolagus
38	481	14.9	92	11	Q8R503	08R503 mus musculu
39	362.5	11.2	539	10	Q22252	022252 arabidopsi
40	291	9.0	263	5	Q8WPE2	08WPE2 porcellio s
41	222	6.9	1130	11	Q91WD8	091WD8 mus musculu
42	205	6.4	1014	6	Q62805	062805 tursiops tr
43	202	6.3	6307	4	Q8WKG9	08WKG9 homo sapien
44	200	6.2	652	5	Q8T8P0	08T8P0 strongyloce
45	187	5.8	4936	16	Q8YKJ3	08YKJ3 anabaena sp

ALIGNMENTS

RESULT 1	
Q96G01	PRELIMINARY: PRT: 924 AA.
ID	Q96G01
AC	Q96G01
DT	01-DEC-2001 (TRENBLREL. 19, Created)
DT	01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT	01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE	Sodium/calcium exchanger SCL8A3.
GN	SCL8A3
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bortoluzzi S.;
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Gabelini N.;
RT	"Characterization of the human SCL8A3 gene for solute carrier family
RT	8, member 3 (sodium/calcium exchanger).";
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ304853; CAC40985.1;
DR	EMBL; AJ304853; CAC40985.1;
DR	InterPro; IPR003644; Calx_beta.
DR	InterPro; IPR004837; NaCa_Exemb.
DR	InterPro; IPR004836; NaCa_Ex.
DR	Pfam; PF03160; Calx_beta; 2.
DR	Pfam; PF01699; NaCa_Ex; 2.
DR	TIGRfams; TIGR00845; Caca; 1.
SO	SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;
Query Match	95.8%; Score 3093; DB 4; Length 924;
Best Local Similarity	100.0%; Pred. No. 3.2e-242;
Matches 595; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAWLRLQPLTSAFLHFGVLTVLFLNGLRARAGSGDVPSTGQNNESCGSSDCKEGVIL 60
DB	1 MAWLRLQPLTSAFLHFGVLTVLFLNGLRARAGSGDVPSTGQNNESCGSSDCKEGVIL 60

```
QY 61 PIWYPENPSLGDKIAIYIYFVALLIYMFVLSIIADRFMAIEVITSOREVYTIKKPNGE 120
DB 61 PIWYPENPSLGDKIAIYIYFVALLIYMFVLSIIADRFMAIEVITSOREVYTIKKPNGE 120
QY 121 TSTTTIRVNNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDGLPSTIVGSAANMFI 180
DB 121 TSTTTIRVNNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDGLPSTIVGSAANMFI 180
QY 181 IIGICVYVPDGETRKIKLRVFEITAAWSIFAYIMYLIAVFSGVQVWEGLLTLFF 240
DB 181 IIGICVYVPDGETRKIKLRVFEITAAWSIFAYIMYLIAVFSGVQVWEGLLTLFF 240
QY 241 FPVCVLLAVAVADKRLLEFYVMHKRYRTDKHKGIIETEGDHPKGIEMDKMNSHFLDGN 300
DB 241 FPVCVLLAVAVADKRLLEFYVMHKRYRTDKHKGIIETEGDHPKGIEMDKMNSHFLDGN 300
QY 301 LVPLEGEVDESREMIIRILKDKOKHPEKDDQLVEMANYALSHQOKSRAFYRIQATR 360
DB 301 LVPLEGEVDESREMIIRILKDKOKHPEKDDQLVEMANYALSHQOKSRAFYRIQATR 360
QY 361 MMTGAGNIIKKHAABQAKKASSMSEVHTDEPDEPFSKVFEDPCSYQCLNCGAVLLTVVR 420
DB 361 MMTGAGNIIKKHAABQAKKASSMSEVHTDEPDEPFSKVFEDPCSYQCLNCGAVLLTVVR 420
QY 421 KGDMSKTYVVDYKTEDGSSANAGADYEFTGTVVLKPGETOKEFSYGIIDDDIFEEDEHF 480
DB 421 KGDMSKTYVVDYKTEDGSSANAGADYEFTGTVVLKPGETOKEFSYGIIDDDIFEEDEHF 480
QY 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTIH 540
DB 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTIH 540
QY 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595
DB 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595

RESULT 2
0960G2 PRELIMINARY: PRT: 925 AA.
AC 0960G2: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabelini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304852; CAC40984.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Extmb.
DR InterPro: IPR004836; NaCa_Ext.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ext; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
SQ SEQUENCE 925 AA; 102803 MW; 0CCF8DA081C4FDA CRC64;
```

Query Match 95.8%; Score 3093; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 3.2e-242;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MAMLRLOPLTSAFLHGLVTVFLFLNGLRAEAGSGDVPSTGONNESCSSSDCKEGLVIL 60
DB 1 MAMLRLOPLTSAFLHGLVTVFLFLNGLRAEAGSGDVPSTGONNESCSSSDCKEGLVIL 60
QY 61 PIWYPENPSLGDKIAIYIYFVALLIYMFVLSIIADRFMAIEVITSOREVYTIKKPNGE 120
DB 61 PIWYPENPSLGDKIAIYIYFVALLIYMFVLSIIADRFMAIEVITSOREVYTIKKPNGE 120
QY 121 TSTTTIRVNNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDGLPSTIVGSAANMFI 180
DB 121 TSTTTIRVNNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDGLPSTIVGSAANMFI 180
QY 181 IIGICVYVPDGETRKIKLRVFEITAAWSIFAYIMYLIAVFSGVQVWEGLLTLFF 240
DB 181 IIGICVYVPDGETRKIKLRVFEITAAWSIFAYIMYLIAVFSGVQVWEGLLTLFF 240
QY 241 FPVCVLLAVAVADKRLLEFYVMHKRYRTDKHKGIIETEGDHPKGIEMDKMNSHFLDGN 300
DB 241 FPVCVLLAVAVADKRLLEFYVMHKRYRTDKHKGIIETEGDHPKGIEMDKMNSHFLDGN 300
QY 301 LVPLEGEVDESREMIIRILKDKOKHPEKDDQLVEMANYALSHQOKSRAFYRIQATR 360
DB 301 LVPLEGEVDESREMIIRILKDKOKHPEKDDQLVEMANYALSHQOKSRAFYRIQATR 360
QY 361 MMTGAGNIIKKHAABQAKKASSMSEVHTDEPDEPFSKVFEDPCSYQCLNCGAVLLTVVR 420
DB 361 MMTGAGNIIKKHAABQAKKASSMSEVHTDEPDEPFSKVFEDPCSYQCLNCGAVLLTVVR 420
QY 421 KGDMSKTYVVDYKTEDGSSANAGADYEFTGTVVLKPGETOKEFSYGIIDDDIFEEDEHF 480
DB 421 KGDMSKTYVVDYKTEDGSSANAGADYEFTGTVVLKPGETOKEFSYGIIDDDIFEEDEHF 480
QY 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTIH 540
DB 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTIH 540
QY 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595
DB 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595

RESULT 3
09EPUB PRELIMINARY: PRT: 595 AA.
AC 09EPUB: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger 3 (Fragment).
GN SLC8A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sokolow S.; Herchenheltz A.; Schurmann S.;
RT "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321404; AAC42826.2; -.
DR MGI; MGI:107976; Slc8a3.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Extmb.
DR InterPro: IPR004836; NaCa_Ext.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ext; 1.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR NON_TER 595
SQ SEQUENCE 595 AA; 66200 MW; 8EF81CBCEDB7854 CRC64;
```

Query Match 93.3%; Score 3012; DB 11; Length 595;
Best Local Similarity 97.5%; Pred. No. 6,4e-236;
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAMRLQPLTSAFLHFGVLTFLVFLNGLRAEAGSGDVPSTGQNNESGSSDCKEYIL 60
Db 1 MAMRLQPLTSAFLHFGVLTFLVFLNGLRAEAGSGDVPSTGQNNESGSSDCKEYIL 60

QY 61 PIWPEPNSLDKTAARVYVYFVALIYMLGYSIADRFMAIEVITTSQEREVTIKKPNGE 120
Db 61 PIWPEPNSLDKTAARVYVYFVALIYMLGYSIADRFMAIEVITTSQEREVTIKKPNGE 120

QY 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHFIAGDLGPGSTIVGSAAFNFI 180
Db 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHFIAGDLGPGSTIVGSAAFNFI 180

QY 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240
Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240

QY 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

QY 301 LVPLEGEKVDSSRRMIRILDLKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360
Db 301 LVPLEGEKVDSSRRMIRILDLKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360

QY 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEPEDFISKVFPDPCSYOCLENGAVLLTYVR 420
Db 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEPEDFISKVFPDPCSYOCLENGAVLLTYVR 420

QY 421 KGDMSKTMVYDYKTEDOSANAGADYEFTEGTVLKPGETOKESVSGIIDDIFEDDEHF 480
Db 421 KGDMSKTMVYDYKTEDOSANAGADYEFTEGTVLKPGETOKESVSGIIDDIFEDDEHF 480

QY 481 FVRLSNVRIEEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIIDDDHAGIIFTECDTIH 540
Db 481 FVRLSNVRIEEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIIDDDHAGIIFTECDTIH 540

QY 541 VSESIGVMEVKVLRISGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595
Db 541 VSESIGVMEVKVLRISGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595

RESULT 4
Q8VHJ8 PRELIMINARY; PRT; 928 AA.

AC Q8VHJ8
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger.
GN SLC8A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SKLEETAL MUSCLE;
RA Kreev A.;
RT "Towards complete inventory of calcium transporters of the house mouse.";
RL Submitted (NCV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF453257; AUJ9160.1; -.
DR MGD: MGI:107976; SLC8a3.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Extmb.
DR InterPro: IPR004836; Na_Ca_Ext.
DR Pfam: PF01699; Na_Ca_Ext; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.

DR SMART: SM00237; Calx_Beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
SO SEQUENCE 928 AA; 102943 MW; A36BBB30BEA123C0 CRC64;

Query Match 93.3%; Score 3012; DB 11; Length 928;
Best Local Similarity 97.5%; Pred. No. 1.2e-235;
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAMRLQPLTSAFLHFGVLTFLVFLNGLRAEAGSGDVPSTGQNNESGSSDCKEYIL 60
Db 1 MAMRLQPLTSAFLHFGVLTFLVFLNGLRAEAGSGDVPSTGQNNESGSSDCKEYIL 60

QY 61 PIWPEPNSLDKTAARVYVYFVALIYMLGYSIADRFMAIEVITTSQEREVTIKKPNGE 120
Db 61 PIWPEPNSLDKTAARVYVYFVALIYMLGYSIADRFMAIEVITTSQEREVTIKKPNGE 120

QY 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHFIAGDLGPGSTIVGSAAFNFI 180
Db 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHFIAGDLGPGSTIVGSAAFNFI 180

QY 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240
Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240

QY 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

QY 301 LVPLEGEKVDSSRRMIRILDLKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360
Db 301 LVPLEGEKVDSSRRMIRILDLKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360

QY 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEPEDFISKVFPDPCSYOCLENGAVLLTYVR 420
Db 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEPEDFISKVFPDPCSYOCLENGAVLLTYVR 420

QY 421 KGDMSKTMVYDYKTEDOSANAGADYEFTEGTVLKPGETOKESVSGIIDDIFEDDEHF 480
Db 421 KGDMSKTMVYDYKTEDOSANAGADYEFTEGTVLKPGETOKESVSGIIDDIFEDDEHF 480

QY 481 FVRLSNVRIEEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIIDDDHAGIIFTECDTIH 540
Db 481 FVRLSNVRIEEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIIDDDHAGIIFTECDTIH 540

QY 541 VSESIGVMEVKVLRISGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595
Db 541 VSESIGVMEVKVLRISGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595

RESULT 5
O97801 PRELIMINARY; PRT; 934 AA.

AC O97801
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger Isoform NCX1.3.
GN NCX1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
CN NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=99175198; PubMed=10075718;
RA Li X.F., Lytton J.;
RT "A circularized sodium-calcium exchanger exon 2 transcript.";
RL J. Biol. Chem. 274:8153-8160(1999).
DR EMBL: AF107593; AAD04173.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.

DR InterPro; IPR004837; NaCa_Exemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx_beta.2.
 DR Pfam; PF01699; Na_Ca_Ex.2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta.2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAL.2; 1.
 SQ SEQUENCE 934 AA; 104331 MW; 2A28DA30254ABC2 CRC64;

Query Match 66.8%; Score 2157; DB 6; Length 934;
 Best Local Similarity 68.7%; Pred. No. 3.5e-166;

Matches 426; Conservative 76; Mismatches 90; Indels 28; Gaps 9;

1 MAMRLQPLTSAFLHGLTVFLF--LNGLRARAGSGDVPSTGONNCGSSGSDCKEGYLPWYPE 58
 1 MRLSLSPFSGNFILLVYVALLFSHVVDVIAETEMEGNGETGE---CTGSYCKKGV 56
 59 ILPIWPNPSSLGDKIARVYVYFVALIYMFGLVSIADRFMASTEVITSOEREVTIKKPN 118
 57 ILPIWEPQDPFGDKIARATVYFVAMVYFGLVSIADRFMSIEVITSOEKETIKKPN 116
 119 GETSTTIVANNVETVNLTLMALGSSAPELLISLIVCGHGFAGDLPSTVYGSAAFM 178
 117 GETTKTVRIWNETVSNLTLMALGSSAPELLISLIVCGHNETAGDLPSTVYGSAAFM 176
 179 FLIIGICVVPIDGERTKIKHLRFVFTAAVSIFAYIMLYMLAVSPGVQVWEGILLT 238
 177 FLIIMACVAVVDPGERIKHLRFVFTAAVSIFATWLIILSVISPGVWEGILLT 236
 239 FFFPVCVLLAMVADKRLFYKTHKKYRTDKHRCIIETEGDHPKG---IEMDGKMMNSH 295
 237 FFFPVCVLLAMVADKRLFYKTHKKYRTDKHRCIIETEGDHPKG---IEMDGKMMNSH 296
 296 ---FLDGNVPLEGKQVVD---ESREMRILKDLKOKPEKLDOLVEMANYALASHOO 348
 297 VENFLDGLV--LEVERDDODEBARREMARILKELKOKPEKLELIELANVOVLSQOO 355
 349 KSRAFYRIQATRMKAGNLIKHAQAOKKASMSSEVHTDEPE-DFISKVFDPSCSYOC 407
 356 KSRAFYRIQATRMKAGNLIKHAQAOKKASMSSEVHTDEPE-DFISKVFDPSCSYOC 415
 408 LENCAGVLLTVYRKGGDKMTYVYKTTEDGSAKNAGADYEFTEGIVYVLRPGEQKFSVG 467
 416 LENCAGVALLTIIRGGDLNTVFDPRTEGAGNAGSDYEFTEGIVYVLRPGEQKFSVG 475
 468 IIDDIDFEEDHEFVRLSNVRIEEOPEEGMPAIFNSLPRLPRAVLASCVANTLDD 527
 476 IIDDIDFEEDHEFVRLSNVRIEEOPEEGMPAIFNSLPRLPRAVLASCVANTLDD 532
 528 HAGIFTECDTHVSEISIGVMEYKVLRTSGARGTVLPFRTEGTAAGGDEPDTYGET 587
 533 HAGIFTECDTHVSEISIGVMEYKVLRTSGARGTVLPFRTEGTAAGGDEPDTYGET 592
 588 EFKNDFTV-----CDROE 600
 593 EFKNDFTV-----CDROE 612

RESULT 6

Q28662 PRELIMINARY; PRT; 941 AA.

AC Q28662; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Renal Na/Ca exchanger NACA-2.
 GN NCX1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TextID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=92321271; PubMed=1621815;
 RA Rellly R.F., Shugrue C.A.;
 RT "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";
 RL Am. J. Physiol. 262:F1105-F1109(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Rellly R.F., Shugrue C.A.;
 RL Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U52665; AAA97928.1;
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DNAL_N.
 DR InterPro; IPR004837; NaCa_Exemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx_beta.2.
 DR Pfam; PF01699; Na_Ca_Ex.2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta.2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAL.2; 1.
 SQ SEQUENCE 941 AA; 105128 MW; 7E11396DE70A4084 CRC64;

Query Match 66.8%; Score 2156.5; DB 6; Length 941;
 Best Local Similarity 68.8%; Pred. No. 3.9e-166;

Matches 421; Conservative 77; Mismatches 87; Indels 27; Gaps 9;

8 PLTSAFLHGLTVFLF--LNGLRARAGSGDVPSTGONNCGSSGSDCKEGYLPWYPE 66
 9 PFSMGHLLAIVLAFRRDHDVSAETEMEGNETGE---CTGSYCKKGVLPWYPE 64
 67 NFSLGRKARVYVYFVALIYMFGLVSIADRFMASTEVITSOEREVTIKKPNGETSTTTI 126
 65 DSGFGKIRARVYFVAMVYFGLVSIADRFMSIEVITSOEKETIKKPNGETTKTV 124
 127 RWNNEFVSNLTLMALGSSAPELLISLIVCGHGFAGDLPSTVYGSAAFMFLIIGIV 186
 125 RWNNEFVSNLTLMALGSSAPELLISLIVCGHGFAGDLPSTVYGSAAFMFLIIGIV 184
 187 YVDPGETKIKHLRFVFTAAVSIFAYIMLYMLAVSPGVQVWEGILLTFFPVCV 246
 185 YVDPGETKIKHLRFVFTAAVSIFAYIMLYMLAVSPGVQVWEGILLTFFPVCV 244
 247 LAMVADKRLFYKTHKKYRTDKHRCIIETEGDHPKG---IEMDGKMMNSH---FLDGN 300
 245 LAMVADKRLFYKTHKKYRTDKHRCIIETEGDHPKG---IEMDGKMMNSH---FLDGN 304
 301 LVPLEGEVD---ESREMRILKDLKOKPEKLDOLVEMANYALSHQOKSRAFYRI 356
 305 LV-LVDERDDODEBARREMARILKELKOKPEKLELIELANVOVLSQOOSRAFYRI 363
 357 OATRMKAGNLIKHAQAOKKASMSSEVHTDEPE-DFISKVFDPSCSYOCLENGCAVL 415
 364 OATRMKAGNLIKHAQAOKKASMSSEVHTDEPE-DFISKVFDPSCSYOCLENGCAVL 423
 416 LTVYRKGGDKMTYVYKTTEDGSAKNAGADYEFTEGIVYVLRPGEQKFSVGIIIDDIDFE 475
 424 LTVYRKGGDKMTYVYKTTEDGSAKNAGADYEFTEGIVYVLRPGEQKFSVGIIIDDIDFE 483
 476 EDEHFFVRLSNVRIEEOPEEGMPAIFNSLPRLPRAVLASCVANTLDDHAGIFTE 535
 484 EDEHFFVRLSNVRIEEOPEEGMPAIFNSLPRLPRAVLASCVANTLDDHAGIFTE 540
 536 CDTIHVSEISIGVMEYKVLRTSGARGTVLPFRTEGTAAGGDEPDTYGETLKNDETV 595
 541 ESVTHVSEISIGVMEYKVLRTSGARGTVLPFRTEGTAAGGDEPDTYGETLKNDETV 600
 596 -----CDROE 600
 601 KIITIRIPDRE 612

RESULT 7
ID Q9TV05 PRELIMINARY: PRT: 602 AA.
AC Q9TV05;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sodium-calcium exchanger circular exon 2 transcript.
GN NCX1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=99175198; PubMed=10075718;
LA X.F., Lytton J.;
LA "A circularized sodium-calcium exchanger exon 2 transcript.";
RL J. Biol. Chem. 274:8153-8160(1999).
DR EMBL; AF109888; AAD04174.1;
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; Naca_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; Na_Ca_Ex; 1.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
SQ SEQUENCE 602 AA; 67369 MW; F46C6BD8D1D32040E CRC64;
Query Match 66.7%; Score 2154.5; DB 6; Length 602;
Best Local Similarity 69.6%; Pred. No. 2.9e-166;
Matches 423; Conservative 75; Mismatches 89; Indels 21; Gaps 8;
DB 1 MAMLUOPLTSAFLHFGVLTFLVLF--LNGLRAGSGDVPSTGQNNESGSSDCKEYV 58
1 MRLSLSPFSGHFLVLAFLFHVVDVLAETEMEGENETGE---CTGSYYCKKGV 56
DB 59 ILPIWYENPNSLGDRIARYIVYFVALIYMFGLGSIADRFNASIVITSOEREVTIKKP 118
57 ILPIWEPQDSFGDKIARATVYFVAMVYMFGLGSIADRFNASIVITSOEREVTIKKP 116
DB 119 GETSTTTIRWNETVSNLTALAGSSAPEILLSLIEVCGHGFIAADLGPSTIVGSAAFNM 178
117 GETTQTVRIMNETVSNLTALAGSSAPEILLSLIEVCGHGFIAADLGPSTIVGSAAFNM 176
DB 179 FIITIGCVVYIPDGETRRIKHLRFVETIAWMSIFAYITWLTMLAVFSPGVVWEGLLTL 238
177 FIITLCVYVVPDGETRRIKHLRFVETIAWMSIFAYITWLTMLAVFSPGVVWEGLLTL 236
DB 239 FFFPYCVLAWVADRRLLFYKYMKHKKRTDKHGIITETGDPKG---IENDGKMMNSH 295
237 FFFPYCVLAWVADRRLLFYKYMKHKKRTDKHGIITETGDPKG---IENDGKMMNSH 296
DB 236 ---FLDGNLVLEGEVD---ESRREMRILDKOKHPEKDLDOLEVAMNYALSHOO 348
237 VENFLDGLVY-LEVDERDODDEARREMARILKELKOKHPEKDLDOLEVAMNYALSHOO 355
DB 297 VENFLDGLVY-LEVDERDODDEARREMARILKELKOKHPEKDLDOLEVAMNYALSHOO 355
DB 349 KSRAFYRQATFMTMGAGILKKHAAEOAKKASSMEVETDEPE-DETSKVFEDCSYOC 407
366 KSRAFYRQATFMTMGAGILKKHAAEOAKKASSMEVETDEPE-DETSKVFEDCSYOC 415
DB 408 LENCAGVLLTVVRKGDMSKTMVYDYKTEDGSANAGADYEFTGTVVLKPGCTOKFEFSG 467
416 LENCAGVLLTVVRKGDMSKTMVYDYKTEDGSANAGADYEFTGTVVLKPGCTOKFEFSG 475
DB 468 IIDDIFEEDEHFFVRLSNVRIIEEQPEEGMPALFNSILPRAYLASCVATVITLDD 527
476 IIDDIFEEDEHFFVRLSNVRIIEEQPEEGMPALFNSILPRAYLASCVATVITLDD 532

528 HAGITFECDTTHVSESGVMEVKLRTSGARGTVVFPRTVEGTAKGGEDEEDTGYEL 587
533 HAGITFECDTTHVSESGVMEVKLRTSGARGTVVFPRTVEGTAKGGEDEEDTGYEL 592
DB 588 EFKNDETV 595
DB 593 EFKNDETV 600
RESULT 8
ID Q9TS14 PRELIMINARY: PRT: 941 AA.
AC Q9TS14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE NA/CA exchanger isoform NACA6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94148976; PubMed=8106495;
RX Kofuji P., Lederer W.J., Schulze D.H.;
RT "Mutually exclusive and cassette exons underlie alternatively spliced
isoforms of the Na/CA exchanger."
LA J. Biol. Chem. 269:5145-5149(1994).
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; Naca_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
SQ SEQUENCE 941 AA; 104995 MW; AEC76774E9E81815 CRC64;
Query Match 66.2%; Score 2136.5; DB 6; Length 941;
Best Local Similarity 69.5%; Pred. No. 1.6e-164;
Matches 417; Conservative 76; Mismatches 86; Indels 21; Gaps 9;
DB 8 PLTSAFLHFGVLTFLVLF--LNGLRAGSGDVPSTGQNNESGSSDCKEYVILPIWPE 66
9 PLSMGFHLAIVLAFEFRRVDHVSATETMEGENETGE---CTGSYYCKKGVILPIWPE 64
DB 67 NPSLGDRIARYIVYFVALIYMFGLGSIADRFNASIVITSOEREVTIKKPGETSTTI 126
65 DPSFGDKIARATVYFVAMVYMFGLGSIADRFNASIVITSOEREVTIKKPGETSTTI 123
DB 127 RYWNETVSNLTALAGSSAPEILLSLIEVCGHGFIAADLGPSTIVGSAAFNMFIILGCV 186
124 RYWNETVSNLTALAGSSAPEILLSLIEVCGHGFIAADLGPSTIVGSAAFNMFIILGCV 183
DB 187 YVYIPDGETRRIKHLRFVETIAWMSIFAYITWLTMLAVFSPGVVWEGLLTLFFPYCVL 246
184 YVYIPDGETRRIKHLRFVETIAWMSIFAYITWLTMLAVFSPGVVWEGLLTLFFPYCVL 243
DB 247 LAMVADRRLLFYKYMKHKKRTDKHGIITETGDPKG---TEMGKMMNSH---FLDGN 300
244 LAMVADRRLLFYKYMKHKKRTDKHGIITETGDPKG---TEMGKMMNSH---FLDGN 303
DB 301 LVLPEGEVD---ESRREMRILDKOKHPEKDLDOLEVAMNYALSHOOKSRAFYRI 356
304 LVLPEGEVD---ESRREMRILDKOKHPEKDLDOLEVAMNYALSHOOKSRAFYRI 362
DB 357 QATRMATGAGILKKHAAEOAKKASSMEVETDEPE-DETSKVFEDPSYOCLEMGAVL 415
363 QATRMATGAGILKKHAAEOAKKASSMEVETDEPE-DETSKVFEDPSYOCLEMGAVL 422
DB 416 LTVVRKGDMSKTMVYDYKTEDGSANAGADYEFTGTVVLKPGCTOKFEFSG 475

```
DB 423 LTIIRRGDGLTNTVFYDFREDGTANAGSDYEFTEGVVFCPEFOKEIRVGIIDDDIFE 482
QY 476 EDHFPRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCVATYIIIDDDAGITFE 555
DB 483 EDNLFVLSNVVSVSTSESDGLENNHS--TLACLSGSPCTRAYITFDDHAGITFE 539
QY 536 CDTIHVSESIGVMEVKVLRISGARGTVIVPRTVEGTAKGGDEDTYGELEFKNDY 595
DB 540 ESVTHVSESIGVMEVKVLRISGARGTVIVPRTVEGTAKGGDEDTYGELEFKNDY 539

RESULT 9
ID 09R238 PRELIMINARY: PRT: 934 AA.
AC 09R238:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Na+/Ca2+-exchanging protein.
OS Rattus norvegicus (Rat).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=DAHL/RAPP R SPRAGUE-DAWLEY;
RA Unlap M.T., Bell P.D.;
RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF109163; AAD23386.1;
DR Interpro: IPR003644; Calx_beta.
DR Interpro: IPR001623; Dnal_N.
DR Interpro: IPR004837; NaCa_Exmemb.
DR Interpro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta.2.
DR Pfam: PF01699; Na_Ca_Ex.2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta.2.
DR TIGRfams: TIGR00845; caca.1.
DR PROSITE: PS50076; Dnal_2.1.
SQ SEQUENCE 934 AA; 104166 MW; C04ED08A75633DDC CRC64;

Query Match 66.1%; Score 2133; DB 11; Length 934;
Best Local Similarity 67.9%; Pred. No. 3.1e-164;
Matches 424; Conservative 72; Mismatches 88; Indels 40; Gaps 10;

QY 4 LRLQPLTSAFLHGLVTFVFL-----NGLRAGSGSDVPSTGQNNESGSSGSDCK 55
DB 2 LRLSLPPNVMGFRVLTVLALFTVHDHTADTEAETGG-----ETTECTGSYYCK 53

QY 56 EGVILPWIWPNPENSGLDKARIVYFVALIYMLGVSIADRPMASIEVITSOEREVTK 115
DB 54 KGVILPWIWPNPENSGLDKARIVYFVALIYMLGVSIADRPMASIEVITSOEREVTK 113

QY 116 KPNGETSTTIRVWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDGPSTIVGSA 175
DB 114 KPNGETSTTIRVWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDGPSTIVGSA 173

QY 176 FNNFIIGICVYVPDGERFKIKHLVFFTTAMSIFFATYIWLMIIVAVSPGVVWEG 235
DB 174 FNNFIIGICVYVPDGERFKIKHLVFFTTAMSIFFATYIWLMIIVAVSPGVVWEG 233

QY 236 LTFEFPVCVLLAWVADKRLLFYKMHKKYRTDKHNGIITTEGDHPKG--TEMGKMM 292
DB 234 LTFEFPVCVLLAWVADKRLLFYKMHKKYRTDKHNGIITTEGDHPKG--TEMGKMM 293

QY 293 NSH---FLOGNLVPLGKEND---ESRREMIILDKOKHPEKLDQVEMANYAAS 345
DB 294 NSH---FLOGNLVPLGKEND---ESRREMIILDKOKHPEKLDQVEMANYAAS 345

QY 346 HOOKSRAFYRIQATRMWTGAGNLIKRAAEQAKKASSMEVHTDEP-DFTSKVFPDPS 404
```

```
DB 353 OOKSRAFYRIQATRMWTGAGNLIKRAAEQAKKASSMEVHTDEP-DFTSKVFPDPS 412
QY 405 YOCLENGAALLVVRKGGMSKTMVVDYKTEGSGNAGGADYFETGTVYLKRGFOKE 464
DB 413 YOCLENGAALLVVRKGGMSKTMVVDYKTEGSGNAGGADYFETGTVYLKRGFOKE 472
QY 465 SVGIIDDDIFEEDHEHFFVRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCVATY 523
DB 473 SVGIIDDDIFEEDHEHFFVRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCVATY 528

QY 524 LDDHAGITFEEDCTIHVSESIGVMEVKVLRISGARGTVIVPRTVEGTAKGGDEDT 563
DB 529 FDDHAGITFEEDCTIHVSESIGVMEVKVLRISGARGTVIVPRTVEGTAKGGDEDT 588

QY 584 YGELEFKNDY-----CDROE 600
DB 589 YGELEFKNDY-----CDROE 612

RESULT 10
ID 09W030 PRELIMINARY: PRT: 934 AA.
AC 09W030:
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Na+/Ca2+-exchanging protein.
OS Rattus norvegicus (Rat).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RA Unlap M.T., Bell P.D.;
RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF109166; AAD23389.1;
DR Interpro: IPR003644; Calx_beta.
DR Interpro: IPR001623; Dnal_N.
DR Interpro: IPR004837; NaCa_Exmemb.
DR Interpro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta.2.
DR Pfam: PF01699; Na_Ca_Ex.2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta.2.
DR TIGRfams: TIGR00845; caca.1.
DR PROSITE: PS50076; Dnal_2.1.
SQ SEQUENCE 934 AA; 104210 MW; 054D06E9179098B5 CRC64;

Query Match 66.0%; Score 2131; DB 11; Length 934;
Best Local Similarity 67.8%; Pred. No. 4.5e-164;
Matches 423; Conservative 73; Mismatches 88; Indels 40; Gaps 10;

QY 4 LRLQPLTSAFLHGLVTFVFL-----NGLRAGSGSDVPSTGQNNESGSSGSDCK 55
DB 2 LRLSLPPNVMGFRVLTVLALFTVHDHTADTEAETGG-----ETTECTGSYYCK 53

QY 56 EGVILPWIWPNPENSGLDKARIVYFVALIYMLGVSIADRPMASIEVITSOEREVTK 115
DB 54 KGVILPWIWPNPENSGLDKARIVYFVALIYMLGVSIADRPMASIEVITSOEREVTK 113

QY 116 KPNGETSTTIRVWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDGPSTIVGSA 175
DB 114 KPNGETSTTIRVWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDGPSTIVGSA 173

QY 176 FNNFIIGICVYVPDGERFKIKHLVFFTTAMSIFFATYIWLMIIVAVSPGVVWEG 235
DB 174 FNNFIIGICVYVPDGERFKIKHLVFFTTAMSIFFATYIWLMIIVAVSPGVVWEG 233

QY 236 LTFEFPVCVLLAWVADKRLLFYKMHKKYRTDKHNGIITTEGDHPKG--TEMGKMM 292
```

Db 224 LTFEFPICVAVAWADRLLEFKYKVRKRYRAGKRGMIIEHEDGRPAKSTEIENDGVV 293
Qy 293 NSH---FLDGNLPLEGKVD---ESRREMIRILDKOKHPEKDOLQVEMANYALS 345
Db 294 NSHVNFLDGNLALY-LEVERRODDDEARREMARILKELKOKHPDKEIOLIELANYOYLS 352
Qy 346 HOOKSRARYRIOATRLMTGAGNILKRNHAAEQAKKSSSEVHTDPE-DFISKVFPDCCS 404
Db 353 OOKSRARYRIOATRLMTGAGNILKRNHAAEQAKKSSSEVHTDPE-DFISKVFPDCCS 412
Qy 405 YOCLENCGAVLLTVVRKGGDSKTMVVDYKTEGDSANAGADYEFTGTVLKPGETOKEF 464
Db 413 YOCLENCGAVLLTVVRKGGDLNTVYVDFRTEDGTANAGSDYFTGTVLKPGETOKEI 472
Qy 465 SVGIIDDDIFEEDEHFFVRLSNVRIEEOPEEGMPAIFNSLPLPR-AVLASPCVATYTI 523
Db 473 RVGIIDDDIFEEDEHFFVRLSNVRSSEVSEDEG---ILDSNHVSALICLSPNATITTI 528
Qy 524 LDDHAGITFECDTIHVSSEIGVMEVYVLRSGARGVYVPRVEGTAKGGGDFEDT 583
Db 529 FDDHAGITFECDTIHVSSEIGVMEVYVLRSGARGVYVPRVEGTAKGGGDFEDT 588
Qy 584 YGELEFKNDETV-----CDROE 600
Db 589 CGELEFONDEIVKTIITIRIFREE 612

RESULT 11

Q9R239 PRELIMINARY: PRT: 957 AA.
Q9R239
AC 09R239: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Na+/Ca2+-exchanging protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DAHL/RAPP S SPRAGUE-DAWLEY;
RA Unlap M.T., Bell P.D.;
RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."
EMBL: AF109164; AAD23387.1;
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ex; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
SQ SEQUENCE 957 AA; 106724 MW; 7A1A6630451EAA7E CRC64;

Query Match 66.0%; Score 2129; DB 11; Length 957;
Best Local Similarity 67.8%; Pred. No. 6.8e-164;
Matches 423; Conservative 72; Mismatches 89; Indels 40; Gaps 10;

Qy 4 LRLDPLTSAFLHGLVTVFLP-----NGLRAAGSGSDVPSTGONNESCSSSDCK 55
Db 2 LRLSLPPLVMSGFLVTLVALLFTVHDHITADTEAETGSGN-----ETTECTGTSYCK 53
Qy 56 EGVLPYIPYEPKPSLGDRIARYIVFVALIYFLVGIITADPFMASIEYVTSQEREVITK 115
Db 54 KGVILPIPEPDPSPGDIARIATVYFAMVYFLGVSIADPFMSIEYVTSQEREVITK 113
Qy 116 KPNGETSTTTIVWNEVYSNLTLMALGSSAPEILLSLIEVCGHFLAGDLGSTIVGSA 175

Db 114 KPNGETSTTTIVWNEVYSNLTLMALGSSAPEILLSLIEVCGHNTPADDLGSTIVGSA 173
Qy 176 FMFIIIGICVYVDPGETRKIKHLRVEFTPAASIFAYIMLYMLAVSPGVVOVWEG 235
Db 174 FMFIIIGICVYVDPGETRKIKHLRVEFTPAASIFAYIMLYMLAVSPGVVOVWEG 233
Qy 236 LTFEFPICVAVAWADRLLEFKYKMKYRDKRGIIIEHEDGPHKG---IENDGVV 292
Db 234 LTFEFPICVAVAWADRLLEFKYKVRKRYRAGKRGMIIEHEDGRPAKSTEIENDGVV 293
Qy 293 NSH---FLDGNLPLEGKVD---ESRREMIRILDKOKHPEKDOLQVEMANYALS 345
Db 294 NSHVNFLDGNLALY-LEVERRODDDEARREMARILKELKOKHPDKEIOLIELANYOYLS 352
Qy 346 HOOKSRARYRIOATRLMTGAGNILKRNHAAEQAKKSSSEVHTDPE-DFISKVFPDCCS 404
Db 353 OOKSRARYRIOATRLMTGAGNILKRNHAAEQAKKSSSEVHTDPE-DFISKVFPDCCS 412
Qy 405 YOCLENCGAVLLTVVRKGGDSKTMVVDYKTEGDSANAGADYEFTGTVLKPGETOKEF 464
Db 413 YOCLENCGAVLLTVVRKGGDLNTVYVDFRTEDGTANAGSDYFTGTVLKPGETOKEI 472
Qy 465 SVGIIDDDIFEEDEHFFVRLSNVRIEEOPEEGMPAIFNSLPLPR-AVLASPCVATYTI 523
Db 473 RVGIIDDDIFEEDEHFFVRLSNVRSSEVSEDEG---ILDSNHVSALICLSPNATITTI 528
Qy 524 LDDHAGITFECDTIHVSSEIGVMEVYVLRSGARGVYVPRVEGTAKGGGDFEDT 583
Db 529 FDDHAGITFECDTIHVSSEIGVMEVYVLRSGARGVYVPRVEGTAKGGGDFEDT 588
Qy 584 YGELEFKNDETV-----CDROE 600
Db 589 CGELEFONDEIVKTIITIRIFREE 612

RESULT 12

Q912J7 PRELIMINARY: PRT: 600 AA.
Q912J7
AC 0912J7: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium-calcium exchanger (Fragment).
GN SLC8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RA Koushik S.V., Conway S.J.;
RT "Role of Sodium Calcium Exchanger During Embryonic Heart Development."
EMBL: AF423306; AAL18847.1;
DR MGI: MGI:107956; SLC8a1.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ex; 1.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
SQ NON-TER 600 AA; 66918 MW; 0307B0A126287247 CRC64;

Query Match 65.9%; Score 2128.5; DB 11; Length 600;
Best Local Similarity 68.7%; Pred. No. 3.7e-164;
Matches 414; Conservative 76; Mismatches 98; Indels 15; Gaps 6;

OY		4	LRLDGLTSAFLHFGIAGTVTLVLRRAEAGSGGSPVPSCGNNESSSSSSKREVIPIW	63
Dd		2	LRLSLRPANVMGFRVLVALVALLFHSVDHDTADTAELRGNGNETTCSTSYCKKCVILPIW	61
OY		64	YPENDSLCDKJARIVIVFVALIYLWFLGVSIADRFPMASIEVITSQEREVITKKRNGEST	123
Dd		62	EPODFSPEDCKIARATAVVFVAWVYMLGSIIADFFMSIEVITSQEKIRITKKPNEGTT	121
OY		124	TTRIRWNTSVNSLTMALMGSSAPELLISLEVCGHGFAGDLGGSTTVGSAAFMFMFIIG	183
Dd		122	TTVRIRNMTVSNSLTLMALGSSAPELLISLVIEVCGHNFTAGDLGGSTTVGSAAFMFMFI	181
OY		184	ICVVYIPDGERTRIKIKHLRVFEITAMWSIFAYIWLIMLAVFSPGVOWMEGLTLTFEPV	243
Dd		182	LCVVYVPPGEETRKIKHLRVFEVTAAWSIFAATMYLIILSVSPGVWEWEGLLTFEFPPI	241
OY		244	CYLLAWAVDKRLLEFKYHKHKRYPRDKNRGIITEFGDHPGC---IDMDKMMNSH---FL	297
Dd		242	CVWFAMVADRRLLEFKYKYKRTRAGKOGMIIEHGSRPASKTEIENDGKVNSHDNFL	301
OY		298	DGNLPLLEGKEVD----ESREMITRIKLDKOKRPEKDQLQOLVEMANYVALSHQKSRAF	353
Dd		302	DGALV-LEVDERDDODEEARREMARILKELOKHKEIBDIELAYOVLISOQOKRAF	366
OY		354	VRIQTARMGTAGNLTKHAAEQKKAKSSMEVHTDEB-DIFSIVFPDPCTIOCLENG	412
Dd		361	YRIQATRLMTAGNLTKRHADAQRKAVSMHEVMEWAENDPVSKIFEEDGYOCLENG	420
OY		413	AVLLTVVRKGDMSTVVDVKYTDEDSANAGADVETPEGVVLKPGETOKBFYSGITDD	472
Dd		421	TVALTIRMGRGDLSITYVDRTREDGTARNAGSDVEFTEGVITFKPGETOIRNYGITDD	480
OY		473	IPEEDEHFVRLSNVRIEEQPEEGMPAIFNSLPRLRAVLASPCVATVTIILDHAGIF	532
Dd		481	IPEEDENFLVHLSNVRSVSDVSEGI--LESNHASSIACIGSPSTATITIFDDHAGIF	537
OY		533	TPEECOTIHVSESIGMEKVKVLTSGANGTVTPRRTEGRAKSGCEPDPTGSELKND	592
Dd		538	TPEEYTHVSESIGIMEKVKVLTSGARKONTIIPYKTIEGTARGSGEDPEDTGCELPEOND	597
OY		593	ETV 595	
Dd		598	ETV 600	
<hr/>				
RESULT 13				
O9ET74		PRELIMINARY;	PRT; 600 AA.	
ID	O9ET74			
AC	O9ET74			
RT	01-MAR-2001 (TREMBLrel. 16, Created)			
NT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Na/Ca exchanger (Fragment).			
GN	SIC8A1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090.			
RH	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129SV; TISSUE=LIVER;			
RX	MEDLINE=20358717; PubMed=10902911;			
RA	Malinco K., Kuro-O M., Yanaka N., Omori K., Komuro I., Inai Y.,			
NA	Nabeshima Y. ;			
RT	"Isolation and characterization of Na(+)/Ca(2+) exchanger gene and			
RT	splicing isoforms in mice."			
RL	DNA Seq. 11:75-81(2000).			
DR	EMBL; AB030885; BAB08169.1.; -.			
DR	MCD; MGI:107956; SIC8A1.			
DR	InterPro: IPRO03644; Calx.beta.			
DR	InterPro: IPRO01623; DnaJ_N.			
DR	InterPro: IPRO04837; NaCa_Exemb.			
DR	InterPro: IPRO04836; Na_Ca_Ex.			

[illegible]

RT "Cloning and expression of a mesangial cell Na⁺/Ca²⁺ exchanger from
RT Sprague-Dawley rats.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
Subm No. 269220

DR EmBL: A1033598; AAK52507.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; DnaJ_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PSS0076; DNaJ_2; 1.
SQ SEQUENCE 962 AA; 107210 MW; 1AA422ED25964192 CRC64;

Query Match	65.88;	Score 2124;	DB 11;	Length 962;
Best Local Similarity	67.68;	Pred. No. 1.8e-163;		
Matches 422; Conservative	73;	Mismatches 89;	Indels 40;	Gaps 10

Db	2	LRLSLPNNVSGRFLVTLVALLTFVHDHITADIEATGNN-----ETTECTIGSYCK	1
Qy	56	EGVLLPTWIPENBSLGDKIARVIVYVALTYMFLVGSITADRFMASIEVTSQEREVTK	1
Db	54	KGVLLPIWEPQDSFGDKIRATVIVYVAMVYMFGLSITADRFMSIEVTSQEREVTK	1
Qy	116	KPNQETSTTIRIWNENVSUMLTLMALGSSAPPELLSLIEVCHGTAIGDLPSTIVGSA	1
Db	114	KPNQETKTIVRIWNEVSNMLTLMALGSSAPPELLSPVIEVCHGNFTADDLGPIIVGSA	1
Qy	176	FNMETIIGICVYVPOGETKIKHLNRFETAAMSFEAYTMYMLIAVSPVQVWVWGL	2
Db	174	FNMETIITALCYVYVPOGETKIKHLNRFETAAMSIFAYTMYTILTSVSSPEVVEWVGL	2
Qy	236	LTLFEFPVCLLWVADKRLLFYKYMHKKYRTDKHNGIITETGDHPKG---IEMDGKM	2
Db	234	LTLFEFPVCLVFWVADKRLLFYKYKRRAGKQGMIIIEHEDGRPSAKTEIENDKVV	2
Qy	293	NSH---FLDGNLVPLECKEVD---ESRREMRILKDKQKHPEKDLQVEMANYVALS	3
Db	294	NSHDNFDLGNLV-LEVDERDQDDEEREMARILTELKQKHPEKDLQVETELANYVALS	3
Qy	346	HQKSRAPFYRLQATRMVMTGNTLKKHNAEDQAKKASMSSEVYTDDEP-DEISKVFEEDCS	4
Db	353	QOKSRAPFYRLQATRLMTGAGNTLKKHRAADQAKKASMEVMDVDVENDPVSKEVEEGT	4
Qy	405	YQCELENGCAVLLVYVRKKGSSKTYMYVDYKTEBDSGANAGDEYETEGVYLVKPGETOKEF	4
Db	413	YQCELENGCYAALLIIRRGGLDTMYVDYPTDEBGTINMADSDELFEGYIIRPGETOKEI	4
Qy	465	SVGIITDDIIEDEDEHFFVRLSNVRIEEOPEEGGMPALFNSLPDR-AVLASPCVATVTI	5
Db	473	RVGIITDDIIEDEDEHFFVRLSNVRSVSSGSEDS---IDSNHVSIALCIQSPNATYTI	5
Qy	524	LDDDHAGITFFECOTIHVSSISGVMEKYVLRTSGAGCYIVYFPRVYEGAKGGGDEFDT	5
Db	529	FDDDHAGITFFEEBPTVHVSISIGIMEKYVLRTSGAGANNIIPYKTIEGTARGGGEDEFDT	5
Qy	584	YGELEFKNDET-----CDROE 600	
Db	589	CGEELFQNDLEIVKLIITRIEDREE 612	
RESULT 15			
Q9WU29			
ID	Q9WU29	PRELIMINARY;	PRT; 969 AA.
AC	Q9WU29;		
DT	01-NOV-1999 (TREMBlrel. 12, Created)		
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)		
DE	Na+/Ca2+-exchanging protein.		
OC	Rattus norvegicus (Rat).		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;

RN SEQUENCE FROM N.A.
 RP [1]
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Unlap M.T., Bell P.D.:
 RT "cDNA cloning of two Na⁺/Ca²⁺ exchangers in mesangial cells from
 RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBD databases.
 DR EMBL; AF109165; AAD23388.1;
 DR InterPro: IPR003644; Calx.beta.
 DR InterPro: IPR001623; DnalJ.
 DR InterPro: IPR004837; NaCa_Extmemb.
 DR InterPro: IPR004836; Na_Ca_Ex.
 DR Pfam: PF03160; Calx.beta; 2.
 DR Pfam: PF01699; Na_Ca_Ex; 2.
 DR PRINTS: PRO1259; NACAECHNGR.
 DR SMART: SM00237; Calx.beta; 2.
 DR TIGRFAMs: TIGR00845; caca; 1.
 DR PROSITE: PS50076; DNALJ_2; 1.
 SQ SEQUENCE 969 AA; 108037 MW; 1D64F6073D3C9C65 CRC64;

Query Match	65.8%	Score 2124	DB 11	Length 969
Best Local Similarity	67.6%	Pred. No. 1.8e-163		
Matches 422				
Conservative	73	Mismatches 89	Indels 40	Gaps 10

QY	4	ILHLOJUTSAFHLFGUJATVLELF-----NOLRAEAGSGGVSTGONNESCSSSPCK	55
Db	2	LRLSLRPVNSMGFRJLVTLVALLFTHVDHITADTEAETGSGN-----ETTCGSGSYCK	53
QY	56	EGVILPIWPEPNSIGDKIARIYVYFVALIYMFGLSVSIADRFMASIEVITISQREBYIK	11
Db	54	KCVILPIWPEODPSFGDKIARATVYFVMYVMEFGLSVSIADRFMSIEVITISQREBYIK	11
QY	116	KNGETSTTIIWVNETVSNLTLMAJGSSAPILLSLIEVCGHGFIAQDLGSTIVGSA	17
Db	114	KNGETSTTIVKIMETVSNLTLMAJGSSAPILLPSVIEVCGHNTFAGDLGSTIVGSA	17
QY	176	FMMFIIIGICVYVIEDGFRKTKHLRVFFITPAANSIFAYIMLXMLAYFSGVYVWMBGL	23
Db	174	FMMFIIIIACVYVVDGFRKTKHLRVFFVTPAAMSIFAYIMLYILSVSPGVWMBGL	23
QY	236	LTLFFEPYCVLLIWAADRLRLEFYKXMKHKRYTRDKIRGJIIETEGDPHG---IEMDGKMM	29
Db	234	LTFEPFPICVPAWADRLLREYKYVYKRYRAGKORGMIEHBGRPASKTEIENDGVV	29
QY	293	NSH-----LIDGNIVYLEGEVD---ESRREMRILIKDKOKHREKDDLOLVEMAYVALS	34
Db	294	NSHVDFLIDGALV-LEVDRODDDEAREREMKRIILKLOKHPDEILDELLIETLAIQVLS	35
QY	346	HOQKSAFERYIQAOTRMKMGAGNIIKKAHEAQKAKSSMEYHTDPE-DFTSKYFEDPCS	40
Db	353	QOQKSAFERYIQAOTRLMTGAGNIIKLRHAADQARKKAVSNHEVIMADVENDPVSKEFEGGT	41
QY	405	YQCLNCGVLLTVYRKGGDKMTKYVYVKTPEDGASANKADVEPYEGVIVLKPGCTOKF	46
Db	413	YQCLNCGVALLTIIRRGDGLNTYVFDVPRTDGANKMSDYELTEGVIYIKRPGTQKEI	47
QY	465	SVGIIDDDIIEEDHEHFVRLSNVRILEEDPOEGMPPAFNSLPRP-AVLASPCVAVYTI	52
Db	473	RVGIIIDDDIIEEDENFLVHLSNVRVSSGSEDG---LLDSNHVSAIACLSGPNATYTI	52
QY	524	LDDHAGITTEFCDDIIHSESIGVMEVYVLPRTSGARGVYVYFPRVEGTAKGCGDEFDT	58
Db	529	PDDHAGITTFEPEPVTYHSESIGIMEVYVLRKISGARGVYVLPYKIEGTARCGGDEFDT	58
QY	584	YGELEFKNDVY-----CDROE 600	
Db	589	CGELEFONDEIVKTIIRIFDREE 612	

